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**RAW SEQUENCE LISTING**

PATENT APPLICATION: US/10/689,576

DATE: 08/04/2004

TIME: 11:02:11

Input Set : N:\Crf3\RULE60\10689576.raw

Output Set: N:\CRF4\08042004\J689576.raw

**SEQUENCE LISTING**

3 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Alessi, Dario R  
7 (ii) TITLE OF INVENTION: ENZYME  
9 (iii) NUMBER OF SEQUENCES: 35  
11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP  
13 (B) STREET: 39 State Street  
14 (C) CITY: Rochester  
15 (D) STATE: New York  
16 (E) COUNTRY: USA  
17 (F) ZIP: 14614-1310  
19 (v) COMPUTER READABLE FORM:  
20 (A) MEDIUM TYPE: Floppy disk  
21 (B) COMPUTER: IBM PC compatible  
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
25 (vi) CURRENT APPLICATION DATA:  
C--> 26 (A) APPLICATION NUMBER: US/10/689,576  
C--> 27 (B) FILING DATE: 20-Oct-2003  
28 (C) CLASSIFICATION: 435  
C--> 42 (vii) PRIOR APPLICATION DATA:  
31 (A) APPLICATION NUMBER: US/08/943,667  
32 (B) FILING DATE: 03-OCT-1997  
35 (A) APPLICATION NUMBER: GB 9705462.1  
36 (B) FILING DATE: 17-MAR-1997  
39 (A) APPLICATION NUMBER: GB 9712826.8  
40 (B) FILING DATE: 19-JUN-1997  
43 (A) APPLICATION NUMBER: GB 9717253.0  
44 (B) FILING DATE: 15-AUG-1997  
C--> 46 (viii) ATTORNEY/AGENT INFORMATION:  
47 (A) NAME: Braman, Susan J  
48 (B) REGISTRATION NUMBER: 34,103  
49 (C) REFERENCE/DOCKET NUMBER: 87792.97R421  
C--> 51 (ix) TELECOMMUNICATION INFORMATION:  
52 (A) TELEPHONE: 716-262-3640  
53 (B) TELEFAX: 716-262-4133  
55 (2) INFORMATION FOR SEQ ID NO: 1:  
57 (i) SEQUENCE CHARACTERISTICS:  
58 (A) LENGTH: 556 amino acids  
59 (B) TYPE: amino acid  
60 (C) STRANDEDNESS: single  
61 (D) TOPOLOGY: linear

**ENTERED**

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63      (ii) MOLECULE TYPE: protein
64      (iii) HYPOTHETICAL: NO
65      (iv) ANTI-SENSE: NO
66      (vi) ORIGINAL SOURCE:
67          (A) ORGANISM: Homo sapiens
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
69      Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
70      1          5          10          15
71      Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
72      20          25          30
73      Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
74      35          40          45
75      Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
76      50          55          60
77      Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
78      65          70          75          80
79      Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
80      85          90          95
81      Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
82      100          105          110
83      Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
84      115          120          125
85      Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
86      130          135          140
87      Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
88      145          150          155          160
89      Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
90      165          170          175
91      Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
92      180          185          190
93      Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
94      195          200          205
95      Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
96      210          215          220
97      Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
98      225          230          235          240
99      Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
100     245          250          255
101     Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
102     260          265          270
103     Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
104     275          280          285
105     Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys
106     290          295          300
107     Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp
108     305          310          315          320
109     Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu
110     325          330          335
111     Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln

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139          340          345          350
141  Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp
142          355          360          365
144  Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly
145          370          375          380
147  Cys Met Gln Val Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser
148          385          390          395          400
150  Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile
151          405          410          415
153  His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu
154          420          425          430
156  Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp
157          435          440          445
159  His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp
160          450          455          460
162  Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu
163          465          470          475          480
165  Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly
166          485          490          495
168  Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys
169          500          505          510
171  Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro
172          515          520          525
174  Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg
175          530          535          540
177  Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
178          545          550          555
180 (2) INFORMATION FOR SEQ ID NO: 2:
182   (i) SEQUENCE CHARACTERISTICS:
183       (A) LENGTH: 1670 base pairs
184       (B) TYPE: nucleic acid
185       (C) STRANDEDNESS: single
186       (D) TOPOLOGY: linear
188   (ii) MOLECULE TYPE: cDNA to mRNA
190   (iii) HYPOTHETICAL: NO
192   (iv) ANTI-SENSE: NO
194   (vi) ORIGINAL SOURCE:
195       (A) ORGANISM: Homo sapiens
198   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
200 ATGGCCAGGA CCACCAGCCA GCTGTATGAC GCCGTGCCCA TCCAGTCCAG CGTGGTGTGA      60
202 TGTTCTGACC CATCCCCATC AATGGTGAGG ACCCAGACTG AGTCCAGCAC GCCCCTGGC      120
204 ATTCCTGGTG GCAGCAGGCA GGGCCCCGCC ATGGACGGCA CTGCAGCCGA GCCTCGGCCC      180
206 GCGCGCGGCT CCCTGCAGCA TCCCAGCCTC CGCCGCAGCC TCGGAAGAAG CGGCCTGAGG      240
208 ACTTCAAGTT TGGGAAAATC CTTGGGGAAG GCTCTTTTTC CACGGTTGTC CTGGCTCGAG      300
210 AACTGGCAAC CTCCAGAGAA TATGCGATTA AAATTCTGGA GAAGCGACAT ATCATAAAAG      360
212 AGAACAAGGT CCCCTATGTA ACCAGAGAGC GGGATGTCAT GTCGCGCCTG GATCACCCCT      420
214 TCTTTGTTAA GCTTTACTTC ACATTTTCTG ACGACGAGAA GCTGTATTTT GGCCTTAGTT      480
216 ATGCCAAAAA TGGAGAACTA CTTAAATATA TTCGCAAAAT CGGTTTCATTC GATGAGACCT      540
218 GTACCCGATT TTACACGGCT GAGATCGTGT CTGCTTTAGA GTACTTGACG GGCAAGGGCA      600

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220 TCATTCACAG GGACCTTAAA CCGGAAAACA TTTTGTTAAA TGAAGATATG CACATCCAGA      660
222 TCACAGATTT TGGAAACAGCA AAAGTCTTAT CCCCAGAGAG CAAACAAGCC AGGGCCAACT      720
224 CATTTCGTGGG AACAGCGCAG TACGTTTCTC CAGAGCTGCT CACGGAGAAG TCCGCCTGTA      780
226 AGAGTTCAGA CCTTTGGGCT CTTGGATGCA TAATATACCA GCTTGTGGCA GGACTCCCAC      840
228 CATTCCGAGC TGGAAACGAG TATCTTATAT TTCAGAAGAT CATTAAAGTTG GAATATGACT      900
230 TTCCAGAAAA ATTCTTCCCT AAGGCAAGAG ACCTCGTGGA GAAACTTTTG GTTTTAGATG      960
232 CCACAAAGCG GTTAGGCTGT GAGGAAATGG AAGGATACGG ACCTCTTAAA GCACACCCGT     1020
234 TCTTCGAGTC CGTCACGTGG GAGAACCTGC ACCAGCAGAC GCCTCCGAAG CTCACCGCTT     1080
236 ACCTGCCGGC TATGTCGGAA GACGACGAGG ACTGCTATGG CAATTATGAC AATCTCCTGA     1140
238 GCCAGTTTGG CTGCATGCAG GTGTCTTCGT CCTCCTCCTC ACACTCCCTG TCAGCCTCCG     1200
240 ACACGGGCCT GCCCCAGAGG TCAGGCAGCA ACATAGAGCA GTACATTCAC GATCTGGACT     1260
242 CGAACTCCTT TGAAGTGGAC TTACAGTTTT CCGAAGATGA GAAGAGGTTG TTGTTGGAGA     1320
244 AGCAGGCTGG CGGAAACCTT TGGCACCAGT TTGTAGAAAA TAATTTAATA CTAAAGATGG     1380
246 GCCCAGTGGA TAAGCGGAAG GGTTTATTTG CAAGACGACG ACAGCTGTTG CTCACAGAAG     1440
248 GACCACATTT ATATTATGTG GATCCTGTCA ACAAAGTTCT GAAAGGTGAA ATTCCTTGGT     1500
250 CACAAGAACT TCGACCAGAG GCCAAGAATT TTAAACTTTT CTTTGTCCAC ACGCCTAACA     1560
252 GGACGTATTA TCTGATGGAC CCCAGCGGGA ACGCACACAA GTGGTGCAGG AAGATCCAGG     1620
254 AGGTTTGGAG GCAGCGATAC CAGAGCCACC CGGACGCCGC TGTGCAGTGA     1670

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256 (2) INFORMATION FOR SEQ ID NO: 3:

258 (i) SEQUENCE CHARACTERISTICS:

259 (A) LENGTH: 16 amino acids

260 (B) TYPE: amino acid

261 (C) STRANDEDNESS: single

262 (D) TOPOLOGY: linear

264 (ii) MOLECULE TYPE: peptide

266 (iii) HYPOTHETICAL: NO

268 (iv) ANTI-SENSE: NO

270 (v) FRAGMENT TYPE: internal

274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

276 Ala Asn Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu

277 1 5 10 15

280 (2) INFORMATION FOR SEQ ID NO: 4:

282 (i) SEQUENCE CHARACTERISTICS:

283 (A) LENGTH: 10 amino acids

284 (B) TYPE: amino acid

285 (C) STRANDEDNESS: single

286 (D) TOPOLOGY: linear

288 (ii) MOLECULE TYPE: peptide

290 (iii) HYPOTHETICAL: NO

292 (iv) ANTI-SENSE: NO

294 (v) FRAGMENT TYPE: internal

298 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

300 Ala Gly Asn Glu Tyr Leu Ile Phe Gln Lys

301 1 5 10

303 (2) INFORMATION FOR SEQ ID NO: 5:

305 (i) SEQUENCE CHARACTERISTICS:

306 (A) LENGTH: 8 amino acids

307 (B) TYPE: amino acid

308 (C) STRANDEDNESS: single

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309      (D) TOPOLOGY: linear
311      (ii) MOLECULE TYPE: peptide
313      (iii) HYPOTHETICAL: NO
315      (iv) ANTI-SENSE: NO
317      (v) FRAGMENT TYPE: internal
321      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
323      Leu Asp His Pro Phe Phe Val Lys
324      1          5
326 (2) INFORMATION FOR SEQ ID NO: 6:
328      (i) SEQUENCE CHARACTERISTICS:
329          (A) LENGTH: 13 amino acids
330          (B) TYPE: amino acid
331          (C) STRANDEDNESS: single
332          (D) TOPOLOGY: linear
334      (ii) MOLECULE TYPE: peptide
336      (iii) HYPOTHETICAL: NO
338      (iv) ANTI-SENSE: NO
342      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
344      Arg Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln
345      1          5          10
347 (2) INFORMATION FOR SEQ ID NO: 7:
349      (i) SEQUENCE CHARACTERISTICS:
350          (A) LENGTH: 12 amino acids
351          (B) TYPE: amino acid
352          (C) STRANDEDNESS: single
353          (D) TOPOLOGY: linear
355      (ii) MOLECULE TYPE: peptide
357      (iii) HYPOTHETICAL: NO
359      (iv) ANTI-SENSE: NO
361      (v) FRAGMENT TYPE: internal
365      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
367      Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn Ser
368      1          5          10
370 (2) INFORMATION FOR SEQ ID NO: 8:
372      (i) SEQUENCE CHARACTERISTICS:
373          (A) LENGTH: 11 amino acids
374          (B) TYPE: amino acid
375          (C) STRANDEDNESS: single
376          (D) TOPOLOGY: linear
378      (ii) MOLECULE TYPE: peptide
380      (iii) HYPOTHETICAL: NO
382      (iv) ANTI-SENSE: NO
384      (v) FRAGMENT TYPE: internal
388      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
390      Thr Ala Ser Gly Val Ala Glu Thr Thr Asn Cys
391      1          5          10
393 (2) INFORMATION FOR SEQ ID NO: 9:
395      (i) SEQUENCE CHARACTERISTICS:
396          (A) LENGTH: 7 amino acids

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/689,576

DATE: 08/04/2004

TIME: 11:02:12

Input Set : N:\Crf3\RULE60\10689576.raw

Output Set: N:\CRF4\08042004\J689576.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:34 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:46 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:51 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]